

Fig. 5

| | -35 re | egion | | -10 region | # |
|-------|--------------------|--------------------|--------------------|-----------------------|--------------------|
| 1051 | CTTTTTCGG <u>C</u> | <u>ATGAG</u> CAACC | AACATTTTCA | AGG <u>TATCAT</u> C (| CTGATGCGCA- |
| | | | | | |
| 1101 | ATATCGGCAT | CGGTTAGCCA | TAACCATTTT | ACCTGTCCGG | CGGCCTTAAT |
| 1151 | ACCTTGATCA | GATGGTTCGT | GGTGTTGTTA | CCTTGCCGAA | GGGCACCGGT |
| 1201 | AAAAATGTTC | GCGTCGGTGT | TTTCGCCCGT | GGCCCGAAAG | CTGAAGAAGC |
| 1251 | TAAAGCTGCT | GGTGCAGAAG | TTGTCGGCGC | AGAAGACCTG | ATGGAAGCCA |
| | | | | | |
| | | -35 region | | -10 reg | gion |
| 1301 | TTCAGGGCGG | CAGCA <u>TTGAT</u> | <u>T</u> TCGATCGTG | ATGCCCTT <u>TA</u> | <u>TAC</u> TGAAATT |
| | ,, | | | | |
| 1251 | # | | A COA COCTOO | | |
| 1351 | GCCTTGCGCT | GCCATAATGA | AGCAGCCTCC | GGTGTTTTGG (| CAGATTIAAG |
| | | | Shin | e-Dalgarno | |
| 1.401 | CCCTCCCTCA | TTTTCGTgat cc | | J | |
| 1401 | COCTOCCTOA | TTTCOTgat co | iciagagi ciaigaaai | g gagaiicaii | |
| | celZ coding reg | ion→ | | | |
| 1451 | | | agtesteege aaget | tggcc (SEQ ID NO: | 1) |
| 1471 | iaigeciele leliali | egg alaaccalce | agicallege aagel | iggee (SEQ ID NO. | 1) |

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| ATATTTTGATTTTTCAAGAAAGCCTGATATCTTCCAACATCTT T (2) 870 TTGACA TATAAT (SEQ ID NO: 18) GATTTGATCCTCTAGAGTCAACCTGCTTGTTACTCGTGATCCCAT A (4) 870 TTGACA TATAAT (SEQ ID NO: 19) GAGTCAACCTGCTTGTTACTCGTGATCCCATTCACAAGGGCGAA C (1) 832 CTTGAAA CCCCAT (SEQ ID NO: 20) TTACTCGTGATCCCATTCACAAGGGCGAATTAATTCGCCCTT C (3) 838 CCGCCT TATACT (SEQ ID NO: 21) | Position (bp) | -35 | -10 | RNA Start | Proposed δ factors | 8 factor e | 8 factor consensus |
|---|------------------|---|--|--------------|-----------------------|------------|--------------------|
| TTTTCAAGAAAGCCTGA <u>TATCTT</u> CCAACA T CTT T (2) δ^{70} CTAGAGTCAACCTGCTTGT <u>TACTCG</u> TGATCCCAT A (4) δ^{70} GCTTGTTACTCGTGA <u>TCCCAT</u> TCACAAGGGCGAA C (1) δ^{32} | | | | | | -35 | -10 |
| FCTAGAGTCAACCTGCTTGT <u>TACTCG</u> TGATCCCAT (a) 8 ⁷⁰ GCTTGTTACTCGTGA <u>TCCCAT</u> TCACAAGGGCGAA (b) 8 ³² F <u>CCCATT</u> CACAAGGGCGAAT <u>TAATTC</u> GCCCTT (c) 8 ³⁸ | | ATATTT <u>TTGATT</u> TTT (SEQ ID NO: 18) | CAAGAAAGCCTGA <u>TATCTT</u> CCAACA T CTT | T (2) | δ ⁷⁰ | TTGACA | TATAAT |
| GCTTGTTACTCGTGA <u>TCCCCAT</u> TCACAAGGGCGAA C (1) δ^{32} | | GAT <u>TTGATC</u> CTCTA (SEQ ID NO: 19) | GAGTCAACCTGCTTGT <u>TACTCG</u> TGATCCC A T | A (4) | 8 ⁷⁰ | TTGACA | TATAAT |
| F <u>CCCATT</u> CACAAGGGCGAAT <u>TAATTC</u> GCCCTT C (3) 8 ³⁸ CCGCCT | | G <u>AGTCAA</u> CCTGCTI (SEQ ID NO: 20) | 'GTTACTCGTGA <u>TCCCAT</u> TCACAAGGGCGAA | C(1) | 8 ³² | CTTGAAA | CCCCAT |
| | | TTACTCGTGAT <u>CCC</u> (SEQ ID NO: 21) | <u>ATT</u> CACAAGGGCGAAT <u>TAATTC</u> GCC C TT | C (3) | §38 | CCGCCT | TATACT |